



FIGURE 1

## SEQ ID NO: 1

>STAAU\_R009 nucleotide sequence: 1800  
TTGCGAATAGATCAATCGATCATTAAATGAAATAAAAGATAAAACCGACATTTTAGACTTGGTAAAGTGA  
ATATGTAAAAATTAGAAAAAGAGGAGCGCAATTATATAGGTTTGTGTCCTTTTCATGATGAAAAGACAC  
CTTCATTTCAGTTTCTTGAGAGATAAACAAATTTGTCATTGTTTGGTTGTAAGGTTGGCAATGTT  
TTTCAATTTACTCAAGAAATTAAGACATATCATTGTTGAAGCGGTTAAAGAAATTAGTGATAGAGT  
TAATGTGTTGCTGATAGATTGAGGCAACACAATCTAACTCAAATGTTCAAATGCTCTGATGATTAC  
AAATGATTGAAATGCATGAGTTAATACAAGAAATTTATTATTACGCTTTAAACAAGACAGTCGAAGGC  
GAACAAGCATTAACTGACTTACAAGAAGCTGGTTTTACAGATGCGCTTATTAAAGAGCGAGGCAATGG  
CTTTGACCCGATAGCTCACATTTTGTGTCATGATTTTCTTCAAAAAAGGGTTACGATATTGAAATTAG  
CATATGAAGCCGGATATTATACAGTAACGAAGAAAAATTCAGTTATTACGATAGATTTTCGAAATTCGT  
ATTATGTTTCTTTGAAAAATGCGCAAGGAAGAAATTTGGGATATTCAAGTCGAACATATACCGGTC  
AGAACCAAAATACTTAAATAGTCCTGAACACCTATCTTTCAAAAAAGAAAGTTGTTATACAACCTTAG  
ATAAAGCGCGTAAATCAATTAGAAAAATTAGATGAAATCGTATTACTAGAAGGTTTTATGGATGTTATA  
AAATCTGATACTGCTGGCTTGAAGAAAGCTTGTGCAACAATGGGTACACAGTTGTCAGATGAACATAT  
TACTTTTATACGAAGTTTAAATCAAAATATAACATTAAATGTTTGAATGGGGATTTTTCGGGGTAGTGAAG  
CAACACTTAAAAACAGGTCAAAATTTGTTACAGCAAGGCTAAATGTATTGTTATACAATTGCCATCA  
GGCATGATCCGGATGAATACATTGGTAAGTATGGCAACGATGCATTACTGCTTTTGTAAAAATGA  
CAAAAAGTCATTTGTCACATTATAAAGTGAGTATATAAAGATGAAATTGCAACATAATGACCTTTCAT  
ATGACAGCTTATTGAAAGAACTAAGTCATGATATTTCGCTTATGAAATCATCGATTTTGAACAAAAAG  
GCTTTAAATGATGTTGCACCATTTTTCATGTTAGTCCTGAGCAATTAGCAAAATACAATTCAA  
TCAAGCACCAAGCCAATTATTATCCAGAAGATGAGTATGGCGGTTACATTGAACCTGAGCCAATTGGTA  
TGGCACAAATTGACAATTGAGCGCTCAAGAAAAAGCGGAGCGAGCATTTTAAAAACATTTAATGAGA  
GATAAAGATACATTTTAAATATTATGAAAGTGTGTGATAAGGATAACTTCAAAAATCAGCATTTTAA  
ATATGTATTGAAAGTCTTACATGATTTTATGCGGAAAAATGATCAATATAATATCAGTGATGCTGTGC  
AGTATGTTAATTCAAATGAGTTGAGAGAAACATAATTAGCTTAGAACATATAATTTGAAATGACGAA  
CCATATGAAATGAAATGATGATTATGTCATGTTATTATGAAAAAGGACAAAGAAACAAATTGAGTC  
ATTGAATCATAAATTAAGGGAAGCTACAAGGATGGCGGATGAGAATTACAAAAATACTATTTACAGC  
AAATTTGTTGCTAAGAATAAAGAACGCATGTAG

## SEQ ID NO: 2

>STAAU\_R009 amino acid sequence : 599  
LRIDQSIINEIKDKTDILDVSEYVKLEKRGNYIGLCPFHDEKTPSFTVSEDKQICHFCGCKKGGNV  
PQFTQETKDISFVEAVKELGDRNVAVDIEATQSNNSNVQIASDDLQMIEMHLEIQFFYYALTAKTVEG  
EQALTYLQERGFDDALIKERGI GFAPDSSHCHDFLQKKYDIELAYEAGLLSRNEENFSYYDRFRNR  
IMFPLKNAQGRI VGYSGRYYTQGEPKYLNSPETPIFOKRKLLYNLDKARKSIRKLEDEIVLLEGFMDVI  
KSDTFLGNVATMGQLSDHEHITFIRKLTNSITLMDFGDFAGSEATLKTGQNLQOGLNVFVIQLPS  
GLMDPEYIGYGNDAFTAFVKNDKKSFAHYKVSILKDEIAHNDLSYERYLKLKSHDISLMKSSILQOK  
ALNDVAPFFFNVSPEQLANBIQNPAPANYYPEDEYGGYIEPEPIGMAQFDNLSRQEKRAERAPLKLHMR  
DKDFTFLNYYESVDKDNFTNQHFKYVFEVLHDFYAENDQYNISDAVQYVNSNELRETLISLEQYNLND  
PYENEIDDYVNVINEKGQBTIESLNHKLREATRIGDVELQKYLLQYIVAKNKM

FIGURE 3C.

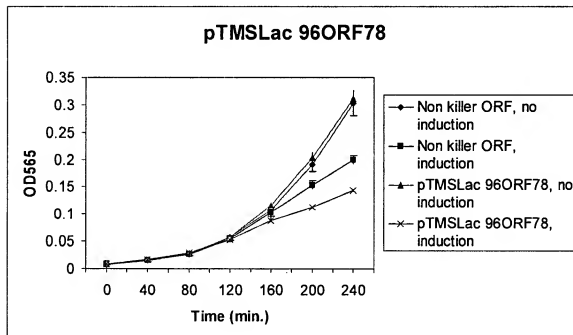
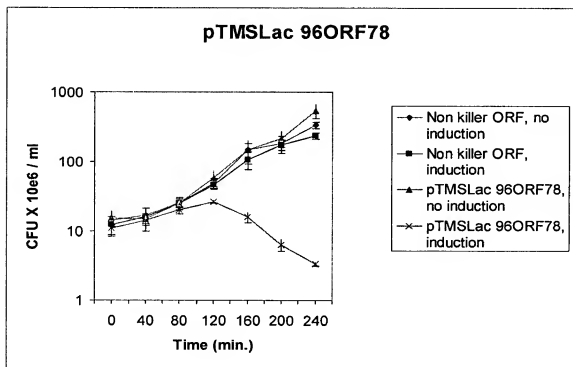


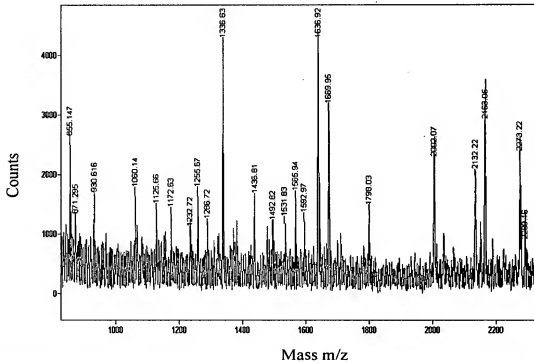
FIGURE 3D.





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FIGURE 6



Details for rank 1 candidate in search 20000916096311-0166-1270000000001

ouContig286: 82020 to 83822: Frame 3 601 aa

Sample ID : orf78 72 [Pass:0]

Measured peptides : 23

Matched peptides : 7

Min. sequence coverage: 14%



Measured Avg/ Computed Error Residues Missed

Mass(M) Mono Mass (Da) Start To Cut Peptide sequence

1124.649	M	1124.622	0.027	588	596	0	YYLQQIVAK
1171.623	M	1171.590	0.033	394	403	0	ELSHDIQLMK
1171.623	M	1171.644	-0.021	5	14	0	IDQSIINEIK
1254.661	M	1254.620	0.041	563	573	0	GQETIESLNHK
1335.627	M	1335.536	0.091	193	202	0	NEENFSYYDR
1435.802	M	1435.734	0.068	233	244	0	YLNSPETPIFOK
1797.019	M	1796.930	0.089	177	192	1	KGYDIELAYEAGLLSR
2001.060	M	2001.016	0.044	374	390	1	VSILKDEIAHNDLSYR

Unmatched Monoisotopic Masses:

855.147 871.295 930.616 1060.140 1232.717 1286.716 1492.822 1531.830 1565.948 1592.967 1636.921 1669.948 2132.217 2163.048 2273.222 2289.164



FIGURE 7A

A. Pfam HMM search results

Model	Seq-from	Seq-to	HMM-from	HMM-to	Score	E-value
zf-CHC2	3	100	1	98	198.4	1.1e-55
Toprim	260	339	1	151	71.9	1.3e-17

Alignments of top-scoring domains:

zf-CHC2:

domain 1 of 1, from 3 to 100: score 198.4, E = 1.1e-55

```

*->ipeesIdeLknriDIVdvisseYVklKkGrnYkgLCPFHdEKTSPSFs
i++++I+e+k+++DI d++seYVkl+K+GrnY+gLCPFHdEKTSPSF+
gi|133988      3      IDQSIINEIKDKTDILDVLVSEYVLEKRGGRNYIGLCPFHdEKTSPSF 49

VspeKqfYhCFGCGagGdaIkFlmkyeklsFvEAveKLADragidlpyek
Vs +Kq+ hCFGC++gG+++ F +++++sFvEAV++L dr+++ ++e
gi|133988     50 VSEDKQICHCFGCKRGGNVFQFTQEIKDIFVFAVKELGDRVNAVVDIEA 99

g<-*
+
gi|133988     100 T      100

```

Toprim: domain 1 of 1, from 260 to 339: score 71.9, E = 1.3e-17

```

*->kvliiVEgpsdakalakalgkpskrkivypggkdgnvaslGhlv
+++++ Eg++d+++ a+ +nvva++G+
gi|133988     260 DEIVLLEGFMDVIKSDTAGL-----KNVVATMGQTQ- 289

dLptpegyddkykwlplpivdvkkgfepyyqiefdqckcskkidlkkeql
l+++e++
gi|133988     290 -----LSDEHI 295

kllklakkadevilatDpDreGeaiawkllellkpygpveeddkkvrr
++kl+++ +l++D+D +G ++++k +l+ +g +v++
gi|133988     296 TFIRKLTSN---ITLMFDGDFAGSEATLKTGQNLQOGL-----NVFV 335

iflp<-*
i+lp
gi|133988     336 IQLP      339

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FIGURE 7B/I

## B. Optimal global alignment of amino acid sequences

Sequence 1 sp|O05338|PRIM\_STAAU\_DNA\_PRIMASE (EC 2.7.7.-) - S. aureus. (572 letters)  
Sequence 2 STAAU\_R009\_STAAU\_R009\_NT|1-1800|(599 letters)

Identical: 560/605 (92%), Similar: 564/605 (93%), Gap: 39/605 (6%)

seq1	1	M-----	1	IGLPFHDEKTPSFTVSEDQKICHCF	27
seq2	1	LRIDQSIINEIKDKIDILDLVSEYKLEKRGNYIGLCPFHDEKTPSFTVSEDQKICHCF	60		
seq1	28	GCKGGNVQFTQEIKDIFSVEAVKELGDRVNVAVDIEATQSNVQIASDDLQWEMHE	87		
seq2	61	GCKGGNVQFTQEIKDIFSVEAVKELGDRVNVAVDIEATQSNVQIASDDLQWEMHE	120		
seq1	88	LIOEYFYVALTIVVEGEQALTYLQERGFDTALIKERGIGFAPDSSHCHDFLOKKGYDIE	147		
seq2	121	LIOEYFYVALTIVVEGEQALTYLQERGFDTALIKERGIGFAPDSSHCHDFLOKKGYDIE	180		
seq1	148	LAYERGLLSNEENFYSYDRFRNIMPLKNAQGRIVGSGRTYTGOEPKYLNSPETPIF	207		
seq2	181	LAYERGLLSNEENFYSYDRFRNIMPLKNAQGRIVGSGRTYTGOEPKYLNSPETPIF	240		
seq1	208	QERKLLYNLDKARKSIRKIDIEIVLLEGFMDVIKSDTAGLKNVATMTGTLSDSEHITPIRK	267		
seq2	241	QERKLLYNLDKARKSIRKIDIEIVLLEGFMDVIKSDTAGLKNVATMTGTLSDSEHITPIRK	300		
seq1	268	LTSNTITLWFDGDFAGSEATLKTQCHLLQQGLNVFVITQLPSGMDPDEYIGKGNDAFTFV	327		
seq2	301	LTSNTITLWFDGDFAGSEATLKTQCHLLQQGLNVFVITQLPSGMDPDEYIGKGNDAFTFV	360		
seq1	328	KNDKKSFAHYKVSILKDEIAHNDLSYERLYKELSHDISLMKSSILQQAINDVAPFNVNS	387		
seq2	361	KNDKKSFAHYKVSILKDEIAHNDLSYERLYKELSHDISLMKSSILQQAINDVAPFNVNS	420		
seq1	388	PEGLANEIQFNQAPANYPEYGYGDIPEPIGMAQFDNLSRREKAEARAFKLHL	447		
seq2	421	PEGLANEIQFNQAPANYPEYGYGDIPEPIGMAQFDNLSRREKAEARAFKLHL	474		



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FIGURE 7B/2



seq1	448	MRDKOTFLNYESVDKNFTNQHFYFVLGHDFYANDQYNISDAQYVNSNELRETLI	507
seq2	475	MRDKOTFLNYESVDKNFTNQHFYFVLGHDFYANDQYNISDAQYVNSNELRETLI	534
seq1	508	SLRQYNLNGSPFENEIDYVNVINEKQETIESLNHKLREATRIGDVELQKYLYQQIVAK	567
seq2	535	SLRQYNLNDPENEIDYVNVINEKQETIESLNHKLREATRIGDVELQKYLYQQIVAK	594
seq1	568	NKERM	572
seq2	595	NKERM	599

Sequence 1 STAAU R009 (599 letters)  
 Sequence 2 gi|9910841|sp|Q9X4D0|PRIM\_BACST DNA PRIVASE(597 letters)

Identical: 209/609 (34%), Similar: 315/609 (51%), Gap: 22/609 (3%)

seq1	1	L-RIDQSIINEIKDKTIDILDVSEYVKLEKGRNIGLCPFHDEKTPSTVSDKQICH	58
seq2	1	MGRIFPETEAIIRRGVDIVDVIGEVQLKRGQENYFGLCPFHGEKTPSTVSPKQIFH	60
seq1	59	CFGCKKGNVFOFTQRIKDISFVEAVKELGDRVNAVDEIATQSNVQIASDDLO-MIE	117
seq2	61	CFCCGAGNAFTFLMDIGEIFVEARKRLAAKAGVDSYVELDVGRDGDGQTDKAKANTE	120
seq1	118	MHELIQFYYALTKTVBQEQALTYLQERFTDALIKERGIGFAPDSSHCFHFLQKGY	177
seq2	121	AHALKRFYHLLVHTKEGQAALDYLAQGWTKETIDRFEIGYAPDAPDAAKLLESHSF	180
seq1	178	DILAYEAGLSEENESYDFRNIMFPLKNAQRIVGYSGRTYTGQEPKYANSPET	237
seq2	181	SLPWMEKAGLLTKKEDG-RYVGRFNRNIMFPHDRGETVGFSGRLLEGCHPKYNSPET	239

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FIGURE 7B/3



seq1	236	PIFOKRLNLDKARKSIRKLEDEITVLLEGFWDIKSDTAGLANVVATGCTOLSDEHITF	297
seq2	240	PVFRKGLLYHFAARVPFRKROEALLVEGFADVISAAQAGIDYAIATMGTSLTESQARI	299
seq1	298	IRKLSNITITMFDGDPAGSEATLKTCQNLLOGLNVFVIQPSGMDPDEYIGKYGNDAFT	357
seq2	300	LRP-CDTITTCVCDGRAGIERAAWAAEQLSALGCRVKVASLPNGLDPDEYINVYGERF-	357
seq1	358	AFVKNDKKSFAHYKVSILKDEIAHNDLSYE----RYLAKELSHDISLAKSSILQOKALNDV	413
seq2	358	AGEACGRPLVAFKWAYLR--RGKNLQHEGERLYIDEALREIGKLSSEVFEQDYILRQL	414
seq1	414	APPFNVSPQLANEIOFNOAPANYPDEYGGYIEPEPIGMAQFONLSROEKABRAFLKH	473
seq2	415	AEFSLSLSALHEQLSRQERTKPREAPDGETARP---MLAKKLLPAPQNAERILLAH	470
seq1	474	LMRDKDFTLNLYESVDKDNFTNQHFYKVFVFLHDPFYAENDQYNISDAVOYVNSNELRETL	533
seq2	471	MWESRDVALVQERIG-GRFNIEEHRALAAVIYAFYEEGHEADPGALISRI-PGELQPLA	528
seq1	534	ISLEQYLNDEPFYENIDYV-NVINEKQGETIESLNHKLREATRIGDVELQKYYLQIV	592
seq2	529	SDVSLLLIADVSEQBLEDYIRHVLNRPKMLKVKEQEKTEAERRKDFLTAARIKEMI	588
seq1	593	AKNK-ERM	599
seq2	589	EMKWLSSS	597







**FIGURE 7B/6**

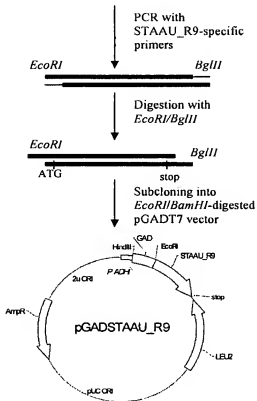
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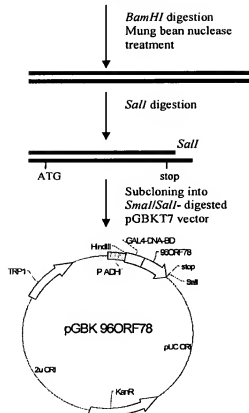
# Replacement Sheet

FIGURE 8

## A- *Staphylococcus aureus* genomic DNA



## B- 96pTMSMLacORF78



## C-

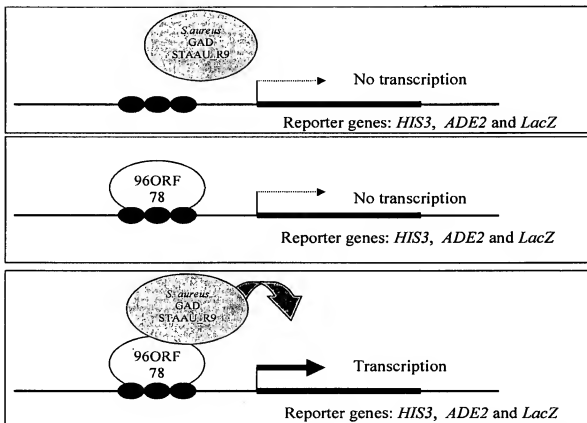
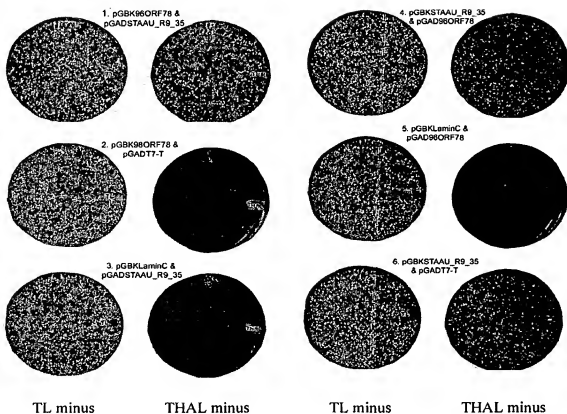


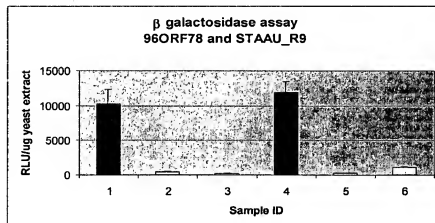


FIGURE 9

A.



B.



Sample	Yeast co-transformants		RLU (avg)	SD
	Plasmid 1	Plasmid 2		
1	pGBK 96ORF78	pGADSTAAU_R9_35	10,250	2,080
2	pGBK 96ORF78	pGADT7-T	475	38
3	pGBK Lamin C	pGADSTAAU_R9_35	224	10
4	pGBKSTAAU_R9_35	pGAD 96ORF78	11,935	1,477
5	pGBK Lamin C	pGAD 96ORF78	243	12
6	pGBKSTAAU_R9_35	pGADT7-T	1,121	37

FIGURE 10

## A. Fragments of STAAU\_R9

Interaction with  
90ORF78

1	599	Yes
35	599	Yes
35	342	No
229	402	No
229	599	Yes
	380	Yes
	380	No
	449	No
	380	No
	490	No
	380	No
	530	No
	380	No
	561	No
	449	Yes
	599	Yes
	400	Yes
	530	Yes
	561	Yes

SEQ ID NO: 6 STAAU\_R9\_561:599  
AMINO ACID SEQUENCE

GQETIESLNHLKRLREATRIGDVELQKYYLQQIVAKNRRN

SEQ ID NO: 5 STAAU\_R9\_1683:1800  
NUCLEIC ACID SEQUENCEGGACAAGAAACAATTGAGTCATGAAATTAAGGGAACTACAAGGATTCGGCATGTA  
GAATTACAAAATACTATTACAGCAAAATTGTTCTTAAGAAATAAAGACCGCATGTAG

## C.

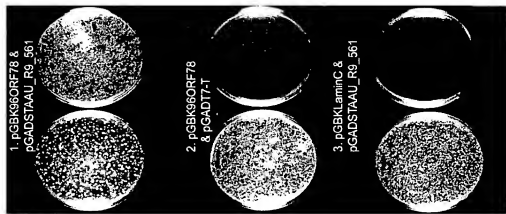




Figure 11 A.

	Primer name	Primer sequence	Restriction site
SEQ ID NO: 8	R9_5E3	5'-ccggaattcTTGCGAATAGATCAATCG-3'	EcoRI
SEQ ID NO: 9	R9_3BG	5'-ggaagatcCTACATGCGTTCTTTATTC-3'	BglII
SEQ ID NO: 10	R9_5E	5'-ccggaattcATGATAGGTTTGTCCT-3'	EcoRI
SEQ ID NO: 11	R9_5E1	5'-ccggaattcCCAAATACCTAAATAGTCC-3'	EcoRI
SEQ ID NO: 12	R9_5E2	5'-ccggaattcGCACATAATGACCTTTCA-3'	EcoRI
SEQ ID NO: 13	R9_342R	5'-cgcggaattccATGCCTGATGGCAATTG-3'	BamHI
SEQ ID NO: 14	R9_402R	5'-ccatcgatGATTTCATAAGCGAAATATC-3'	Clal
SEQ ID NO: 15	R9_449F	5'-ccggaattcCCTGAGCCAATTGGTATGGC-3'	EcoRI
SEQ ID NO: 16	R9_449R	5'-cgcggaattccctaAGGTTCAATGTAACCGCC-3'	BamHI
SEQ ID NO: 17	R9_490F	5'-ccggaattcAAGGATAACTTCACAAATCAG-3'	EcoRI
SEQ ID NO: 18	R9_490R	5'-cgcggaattccctaCTTATCAACACTTTTCATAATA-3'	BamHI
SEQ ID NO: 19	R9_530F	5'-ccggaattcAGAGAAACACTAATTAGCTTA-3'	EcoRI
SEQ ID NO: 20	R9_530R	5'-cgcggaattccctaTCTCAACTCATTTGAATTAAC-3'	BamHI
SEQ ID NO: 21	R9_561F	5'-ccggaattcGGACAAGAAACAATTGAGTC-3'	EcoRI
SEQ ID NO: 7	R9_561R	5'-cgcggaattccctaTCCTTTTCATTAATAACATTG-3'	BamHI

Figure 11 B.

Cloning of SEQ ID NO: 2 amino acid fragments	Sense primer	Antisense primer
1-599	R9_5E3	R9_3BG
35-599	R9_5E	R9_3BG
35-342	R9_5E	R9_342R
229-402	R9_5E1	R9_402R
229-599	R9_5E1	R9_3BG
380-599	R9_5E2	R9_3BG
380-449	R9_5E2	R9_449R
380-490	R9_5E2	R9_490R
380-530	R9_5E2	R9_530R
380-561	R9_5E2	R9_561R
449-599	R9_449F	R9_3BG
490-599	R9_490F	R9_3BG
530-599	R9_530F	R9_3BG
561-599	R9_561F	R9_3BG